Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (*Previously presented*) A method for mass-spectrometric analysis of a known mutation site in genome DNA, the method comprising:

providing an extension primer having a nucleotide chain that contains a photocleavable linker and attaching the primer to the DNA adjacent to the mutation site;

extending the primer using mutation dependent primer extension with a complementary mixture of non-terminating and terminating nucleoside triphosphate derivatives, said mixture having a ratio of one non-terminating to three terminating nucleoside triphosphate derivatives, or two non-terminating to two terminating nucleoside triphosphate derivatives, the terminating nucleoside triphosphate derivatives terminating the extension at one of a plurality of predetermined lengths;

cleaving the photocleavable linker with UV light irradiation to produce a DNA cleavage product; and

analyzing the DNA cleavage product using mass spectrometric analysis to determine the nucleotide present at the mutation site.

2. (*Previously presented*) A method as in Claim 1, wherein the linker is located 3 to 10 bases from the 3' position of the primer.

3. (*Previously presented*) A method as in Claim 1, wherein the linker is derived from the class of chemical compounds known as o-nitrobenzyl derivatives.

4. (*Previously presented*) A method as in Claim 1, wherein the extension is carried out so that extension only takes place by precisely one base.

5. (*Previously presented*) A method as in Claim 4, wherein dideoxynucleoside triphosphates are used as the nucleoside triphosphate derivative terminators.

6. (*Canceled*).

7. (*Previously presented*) A method as in Claim 1, wherein an internucleotide cyanoethyl phosphite bond of the primer nucleotides between the linker and the 3' position is sulphurized forming phosphorothioate nucleotides, and wherein the phosphorothioate nucleotides are alkylated before analysis by mass spectrometry.

8. (*Currently amended*) A method as in Claim 7, wherein the extension is carried out with a complementary mixture of ~~four types of~~ terminating and non-terminating nucleoside triphosphate ~~derivative terminators~~ derivatives and negatively charged ions are measured in the mass spectrometer.

9. (*Previously presented*) A method as in Claim 8, wherein dideoxynucleoside triphosphates are used as nucleoside triphosphate derivative terminators.

10. (*Currently amended*) A method as in Claim 9, wherein the extension is carried out with a complementary mixture of ~~four types of~~ terminating and non-terminating nucleoside triphosphate ~~derivative terminators~~ derivatives in which the nucleotide that is inserted, like the phosphorothioate nucleotides of the primer, is alkylated before analysis by mass spectrometry and the negative ions are measured in the mass spectrometer.

11. (*Previously presented*) A method as in Claim 10, wherein α-thiodideoxynucleoside triphosphates are used as the nucleoside triphosphate derivative terminators.

12. (*Previously presented*) A method as in Claim 11, wherein each one of the α-thionucleoside triphosphate derivative terminators carries a chemical group with a positive charge in addition.

13. (*Previously presented*) A method as in Claim 10, wherein one of the phosphorothioate nucleotides of the extension primer carries a chemical group with a positive charge.

14. (*Previously presented*) A method as in Claim 13, wherein the chemical group carrying the charge is located on the second, third or fourth nucleobase counting from the 3' position.

15. (*Previously presented*) A method as in Claim 12, wherein a chemical group carrying the charge is a quaternary ammonium group.

16. (*Previously presented*) A method as in Claim 10, wherein the primer for the primer extension carries an anchor for the attachment of a charge group which is attached before the analysis by mass spectrometry is carried out.

17. (*Previously presented*) A method as in Claim 16, wherein the anchor carries a free amino group.

18. (*Previously presented*) A method as in Claim 1, wherein ionization in the mass-spectrometric mass determination is achieved by using matrix-assisted laser desorption and ionization (MALDI).

19. (*Previously presented*) A method as in Claim 12, wherein ionization in the mass-spectrometric mass determination is achieved by using matrix-assisted laser desorption and ionization (MALDI), and wherein a matrix is used which does not contribute to the transfer of charge to the DNA products being measured.

20. (*Previously presented*) A method as in Claim 19, wherein α-cyano-4-hydroxycinnamic acid methyl ester is used as the matrix.

21. (*Previously presented*) A method as in Claim 1, wherein the 5' position of the extension primer is biotinylated.

22. (*Previously presented*) A method as in Claim 21, wherein the primer, after extension, is bonded via biotin to a streptavidin molecule that is fixed to a surface for the purpose of purging all the components of reaction fluid that was required for the extension.

23. (*Previously presented*) A method as in Claim 22, wherein the streptavidin is bonded to a surface of a sample support which is also used for further mass-spectrometric analysis.

24. (*Previously presented*) A method for mass-spectrometric analysis of a known mutation site in genome DNA, the method comprising:

providing an extension primer having a nucleotide chain that contains a photocleavable linker and attaching the primer to the DNA adjacent to the mutation site;

extending the primer using mutation dependent primer extension, the primer extension using at least one chain terminator that terminates the extension at one of a plurality of predetermined lengths, wherein the extension uses a complementary mixture of fewer than four non-terminating and terminating nucleoside triphosphate derivatives and is carried out such that the predetermined lengths differ by at least one base;

cleaving the photocleavable linker with UV light irradiation to produce a DNA cleavage product; and

analyzing the DNA cleavage product using mass spectrometric analysis to determine the nucleotide present at the mutation site.

25. (*Previously presented*) A method as in Claim 24, wherein the linker is located 3 to 10 bases from the 3' position of the primer.

26. (*Previously presented*) A method as in Claim 24, wherein dideoxynucleoside triphosphates are used as the nucleoside triphosphate derivative terminators.

27. (*Previously presented*) A method as in Claim 24, wherein the 5' position of the extension primer is biotinylated.

28. (*Previously presented*) A method as in Claim 27, wherein the primer, after extension, is bonded via biotin to a streptavidin molecule that is fixed to a surface for the purpose of purging all the components of reaction fluid that was required for the extension.

29. (*Previously presented*) A method as in Claim 28, wherein the streptavidin is bonded to a surface of a sample support which is also used for further mass-spectrometric analysis.